

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:21:53 ; Search time 45.33 Seconds
(without alignments)
184,420 Million cell updates/sec

Title: US-09-351-778a-10

Sequence score: 87
1 MTSSTIAPTDYNTATGL.....RPPIYPIGLKPCSLLOYD 87

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_71:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	27.6	93	1 ERAD53	early E3a 10.5K pr
2	7	8.0	160	2 C95415	hypothetical prote
3	7	8.0	197	2 C86523	CT142, hypothetical
4	7	8.0	387	2 C89783	hypothetical prote
5	7	8.0	391	2 D97201	aICAR transformla
6	7	8.0	425	2 AC2909	MFS permease [impo
7	7	8.0	487	2 B97684	probable tarttrate
8	7	8.0	536	2 T27668	hypothetical prote
9	7	8.0	965	2 T17395	probable DEAH ATP-
10	7	8.0	1175	2 H83437	hypothetical prote
11	6	6.9	69	2 P80453	adenylate cyclase
12	6	6.9	82	2 D82650	hypothetical prote
13	6	6.9	83	2 G82744	hypothetical prote
14	6	6.9	89	2 D87338	hypothetical prote
15	6	6.9	94	2 E82629	hypothetical prote
16	6	6.9	94	2 D82626	phage-related prot
17	6	6.9	97	2 T40639	hypothetical prote
18	6	6.9	113	2 C81220	hypothetical prote
19	6	6.9	113	2 C81990	hypothetical prote
20	6	6.9	119	2 H83186	hypothetical prote
21	6	6.9	121	2 J01466	nucleic acid-bindl
22	6	6.9	121	2 T31448	cyclochrome bc1 ch
23	6	6.9	126	2 D95915	hypothetical prote
24	6	6.9	128	2 AD1054	conserved hypotet
25	6	6.9	130	2 E70353	hypothetical prote
26	6	6.9	134	2 S52546	thionin variant rh
27	6	6.9	136	2 T23960	hypothetical prote
28	6	6.9	142	2 S32960	hypothetical prote
29	6	6.9	144	2 R33588	high-affinity bran

30	6	6.9	148	2 T03569	hypothetical 16.9K
31	6	6.9	150	2 G87270	general secretion
32	6	6.9	157	2 S75191	hypothetical prote
33	6	6.9	157	2 S35037	helix-loop-helix p
34	6	6.9	157	2 T48683	hypothetical prote
35	6	6.9	160	2 D83575	hypothetical prote
36	6	6.9	170	2 T17286	hypothetical prote
37	6	6.9	174	2 C82129	conserved hypotet
38	6	6.9	176	2 G84436	NAM (no apical mer
39	6	6.9	182	2 H87383	hypothetical prote
40	6	6.9	184	2 I64031	hypothetical prote
41	6	6.9	195	2 E71000	hypothetical prote
42	6	6.9	203	2 T34058	hypothetical prote
43	6	6.9	211	2 T36878	hypothetical prote
44	6	6.9	218	2 S29712	segmentation prote
45	6	6.9	222	2 A75476	response regulator

ALIGNMENTS

RESULT 1
ERAD53
early E3a 10.5K protein - human adenovirus 5
C:Species: Mastadenovirus hs (human adenovirus 5)
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C:Accession: A05245
R:Cladaras, C.; Wold, W.S.M.
Virology 140, 28-43, 1985
A:Title: DNA sequence of the early E3 transcription unit of adenovirus 5.
A:Reference number: A94335; MUID:85092388
A:Accession: A05245
A:Molecule type: DNA
A:Residues: 1-93 <CLIA>
A:Cross-references: GB:X03002; NID:958503; PIDN:CAA26784.1; PID:958507
C:Superfamily: adenovirus early E3a 10.5K protein
C:Keywords: early protein; transmembrane protein

Query Match: 27.6% Score 24; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.9e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMFSLAMFVCLIIIMLICCLR 64
DB 34 MMFSLAMFVCLIIIMLICCLR 57

RESULT 2
C95415
hypothetical protein Sma2279 [Imported] - Sinorhizobium meliloti (strain 1021) magap1
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95415
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95415
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65885.1; PID:914524394; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Publisher, A.; Abola, P.; Ampe, F.; Barloy-Hub
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SWA2279
A:Genome: plasmid

Query Match 8.0%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 TGSTAP 8
Db 28 TGSTAP 34

RESULT 3
C86523
CT12 hypothetical protein_2 [imported] - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86523
R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishl, F.; Ouchi, K.; Shiba, T.; IS
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: C86523
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:BA000008; NID:9878632; PIDN:BA86469.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0259

Query Match 8.0%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
Db 74 ATGLTSA 80

RESULT 4
C89783
hypothetical protein SA0200 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89783
R:Kutoda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, O.; Y., Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:2131952; PMID:11418146
A:Accession: C89783
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-387 <KUR>
A:Cross-references: GB:BA000018; PID:g13700123; PIDN:BA84142.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0200

Query Match 8.0%; Score 7; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 20 LTSALNL 26
|||||||

Db 27 LTSALNL 33

RESULT 5
D97201
aICAR transformylase domain of purH-like protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97201
R:Nolling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; L
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97201
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-391 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80399.1; PID:g15025462; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2445

Query Match 8.0%; Score 7; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
Db 58 ATGLTSA 64

RESULT 6
AC2909
MFS permease [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AC2909
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Hiddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AC2909
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-425 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43689.1; PID:g17741216; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2708
A:Map position: circular chromosome

Query Match 8.0%; Score 7; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTAP 8
Db 390 TGSTAP 396

RESULT 7
B97684
probable tetratrate transporter AGR_C.4908 [imported] - Agrobacterium tumefaciens (stra
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97684

R.Goodner, B.: Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollem, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A:Reference number: A97359; PMID:11743194
 A:Accession: B97684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1487 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AN88427.1; PID:g15157922; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_4908
 A:Map position: circular chromosome

Query Match 8.0%; Score 7; DB 2; Length 487;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 TGSTIAP 8
 Db 452 TGSTIAP 458

RESULT 8
 T27668
 hypothetical protein ZK1053.2 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C:Accession: T27668
 R:Kershaw, J.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z29402
 A:Accession: T27668
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1536 <WIL>
 A:Cross-references: EMBL:Z82084; PIDN:CA804976.1; GSPDB:GN00019; CESP:ZK1053.2
 A:Experimental source: clone ZK1053
 C:Genetics:
 A:Gene: CESP:ZK1053.2
 A:Map position: 1
 A:Introns: 56/3; 88/3; 203/1; 228/2; 383/1; 467/3
 C:Superfamily: *Caenorhabditis elegans* hypothetical protein ZK1053.2

Query Match 8.0%; Score 7; DB 2; Length 536;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 STIAPT 10
 Db 295 STIAPT 301

RESULT 9
 T17395
 probable DEAH ATP-dependent helicase - *Dichelobacter nodosus*
 C:Species: *Dichelobacter nodosus*
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17395
 R:Billington, S.J.; Huggins, A.S.; Johannesen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, M.
 Infect. Immun. 67, 1277-1286, 1999
 A>Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) C
 A:Reference number: Z18734; MUID:99150261
 A:Accession: T17395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-965 <BIL>
 A:Cross-references: EMBL:U20246; NID:93493323; PID:g23117808; PIDN:AC33384.1
 A:Experimental source: strain A198

Query Match 8.0%; Score 7; DB 2; Length 965;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 23 ALNLPDV 29
 Db 772 ALNLPDV 778

RESULT 10
 H83437
 hypothetical protein PA1669 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83437
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lapid, K.; L.
 Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:20437337
 A:Accession: H83437
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1175 <STO>
 A:Cross-references: GB:AE004594; GB:AE004091; NID:g9947630; PIDN:AG05058.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1669

Query Match 8.0%; Score 7; DB 2; Length 1175;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 63 KRRRAP 69
 Db 213 KRRRAP 219

RESULT 11
 P0453
 adenylate cyclase (EC 4.6.1.1) - human (fragment)
 N:Alternate names: adenylyl cyclase
 C:Species: *Homo sapiens* (man)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: P0453
 R:Hellevuo, K.; Yoshimura, M.; Kao, M.; Hoffman, P.L.; Cooper, D.M.F.; Tabakoff, B.
 Biochem. Biophys. Res. Commun. 192, 311-318, 1993
 A>Title: A novel adenylyl cyclase sequence cloned from the human erythroleukemia cell
 A:Reference number: P0453; MUID:93236590
 A:Accession: P0453
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-69 <HEL>
 C:Comment: This enzyme catalyzes the synthesis of adenosin 3',5'-cyclic monophosphate
 C:Superfamily: human adenylyl cyclase; guanylate cyclase catalytic domain homology
 C:Keywords: phosphorus-oxygen lyase
 F.1-69/Domain: guanylate cyclase catalytic domain homology (fragment) <GCC>

Query Match 6.9%; Score 6; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 44 FSIALM 49
 Db 28 FSIALM 33

RESULT 12
 D82630
 hypothetical protein XF1852 [Imported] - *Xylella fastidiosa* (strain 9a5c)

C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: D82630
 R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82630
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-82 <SIN>
 A:Cross-references: GB:AE004006; GB:AE003849; NID:9106932; PIDN:AAF84658.1; GSPDB:GN001
 A:Experimental source: strain 9a5c
 R:Simpton, A.J.G.; Reimach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XFL852

Query Match 6.9%; Score 6; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 KPCSL 83
 |||||
 DB 32 KPCSL 37

RESULT 13
 G82744
 Hypoetical protein XE0934 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: G82744
 R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: G82744
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-83 <SIN>
 A:Cross-references: GB:AE003932; GB:AE003849; NID:9105849; PIDN:AAF3744.1; GSPDB:GN001
 A:Experimental source: strain 9a5c
 R:Simpton, A.J.G.; Reimach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:

A:Gene: XE0934

Query Match 6.9%; Score 6; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 SLLLO 86
 |||||
 DB 4 SLLLO 9

RESULT 14
 D87338
 Hypoetical protein CC0719 [imported] - *Caulobacter crescentus*
 C:Species: *Caulobacter crescentus*
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: D87338
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; DebRoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete genome sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: D87338
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <STO>
 A:Cross-references: GB:AE005673; NID:913421946; PIDN:AAK22704.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0719

Query Match 6.9%; Score 6; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRAP 69
 |||||
 DB 16 RRRAP 21

RESULT 15
 E82629
 Plaque-related protein XFL869 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: E82629
 R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: E82629
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-94 <SIN>
 A:Cross-references: GB:AE004007; GB:AE003849; NID:9106944; PIDN:AAF84675.1; GSPDB:GN
 A:Experimental source: strain 9a5c
 R:Simpton, A.J.G.; Reimach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fr
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, H
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 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
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 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:

C:Genetics:
A:Gene: XF1869

Query Match 6.9%; Score 6; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 TSAIHL 26
DB 39 TSAIHL 44

Search completed: June 21, 2002, 08:21:53
Job time: 98 sec